

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:18:30 ; Search time 124 Seconds
(without alignments)
261.332 Million cell updates/sec

Title: US-10-664-456-12_COPY_389_491
Perfect score: 615
Sequence: 1 VHTKDIFNVKRCNGVVEEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615	100.0	766	12	US-10-664-456-12 Sequence 12, Appl
2	615	100.0	787	12	US-10-664-456-13 Sequence 13, Appl
3	615	100.0	820	12	US-10-664-456-14 Sequence 14, Appl
4	615	100.0	820	16	US-10-408-765A-1252 Sequence 1252, Ap
5	557	90.6	528	9	US-09-792-200B-22 Sequence 22, Appl
6	446	72.5	726	12	US-10-633-202-2 Sequence 2, Appli
7	446	72.5	726	14	US-10-156-028-3 Sequence 3, Appli
8	446	72.5	776	10	US-09-978-418-6 Sequence 6, Appli
9	443	72.0	722	14	US-10-265-125-2 Sequence 2, Appli
10	443	72.0	722	15	US-10-074-978A-288 Sequence 288, App
11	443	72.0	722	15	US-10-074-978A-289 Sequence 289, App
12	431	70.1	446	9	US-09-792-200B-12 Sequence 12, Appl
13	431	70.1	535	12	US-10-633-202-3 Sequence 3, Appli
14	422	68.6	523	9	US-09-792-200B-14 Sequence 14, Appl
15	408	66.3	729	15	US-10-074-978A-287 Sequence 287, App

16	357	58.0	499	12	US-10-664-456-6	Sequence 6, Appli
17	357	58.0	781	12	US-10-664-456-16	Sequence 16, Appl
18	357	58.0	781	15	US-10-074-978A-286	Sequence 286, App
19	357	58.0	790	12	US-10-147-493-204	Sequence 204, App
20	357	58.0	790	12	US-10-145-127-204	Sequence 204, App
21	357	58.0	790	12	US-10-160-503-204	Sequence 204, App
22	357	58.0	790	12	US-10-143-118-204	Sequence 204, App
23	357	58.0	790	12	US-10-144-993-204	Sequence 204, App
24	357	58.0	790	12	US-10-158-787-204	Sequence 204, App
25	357	58.0	790	12	US-10-664-456-15	Sequence 15, Appl
26	357	58.0	790	12	US-10-140-024-204	Sequence 204, App
27	357	58.0	790	12	US-10-140-808-204	Sequence 204, App
28	357	58.0	790	12	US-10-152-405-204	Sequence 204, App
29	357	58.0	790	12	US-10-127-852A-204	Sequence 204, App
30	357	58.0	790	12	US-10-127-900A-204	Sequence 204, App
31	357	58.0	790	12	US-10-128-685A-204	Sequence 204, App
32	357	58.0	790	12	US-10-131-820A-204	Sequence 204, App
33	357	58.0	790	12	US-10-142-886-204	Sequence 204, App
34	357	58.0	790	12	US-10-146-728-204	Sequence 204, App
35	357	58.0	790	12	US-10-146-786-204	Sequence 204, App
36	357	58.0	790	12	US-10-147-499-204	Sequence 204, App
37	357	58.0	790	12	US-10-157-798-204	Sequence 204, App
38	357	58.0	790	14	US-10-028-072-204	Sequence 204, App
39	357	58.0	790	14	US-10-121-049-204	Sequence 204, App
40	357	58.0	790	14	US-10-123-904-204	Sequence 204, App
41	357	58.0	790	14	US-10-140-470-204	Sequence 204, App
42	357	58.0	790	14	US-10-175-746-204	Sequence 204, App
43	357	58.0	790	14	US-10-176-918-204	Sequence 204, App
44	357	58.0	790	14	US-10-176-921-204	Sequence 204, App
45	357	58.0	790	14	US-10-137-865-204	Sequence 204, App

ALIGNMENTS

RESULT 1
US-10-664-456-12
; Sequence 12, Application US/10664456
; Publication No. US20040038364A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
; FILE REFERENCE: 03260.0093-00304
; CURRENT APPLICATION NUMBER: US/10/664,456
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323
; PRIOR FILING DATE: prior FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/116,670
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 60/138,682
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 60/155,798
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 12
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-456-12

Query Match	100.0%;	Score 615;	DB 12;	Length 766;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-49;			
Matches 103;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	VHTKDIFNVKRCNGVVEEGEECDG	PLKHCAKDP	CCLSNCTLTDGSTCA	FGLCKDCKF 60
		</			

RESULT 2
US-10-664-456-13
; Sequence 13, Application US/10664456
; Publication No. US20040038364A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
; TITLE OF INVENTION: DNAS AND POLYPEPTIDES
; FILE REFERENCE: 03260.0093-00304
; CURRENT APPLICATION NUMBER: US/10/664,456
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323
; PRIOR FILING DATE: prior FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/116,670
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 60/138,682
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 60/155,798
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-456-13

Query Match 100.0%; Score 615; DB 12; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.4e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 60
Db 389 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 448

QY 61 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 3
US-10-664-456-14
; Sequence 14, Application US/10664456
; Publication No. US20040038364A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
; TITLE OF INVENTION: DNAS AND POLYPEPTIDES
; FILE REFERENCE: 03260.0093-00304
; CURRENT APPLICATION NUMBER: US/10/664,456
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323
; PRIOR FILING DATE: prior FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/116,670
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 60/138,682
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 60/155,798
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-456-14

Query Match 100.0%; Score 615; DB 12; Length 820;
Best Local Similarity 100.0%; Pred. No. 4.6e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 60
Db 389 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 448

QY 61 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 4
US-10-408-765A-1252
; Sequence 1252, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1252
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1252

Query Match 100.0%; Score 615; DB 16; Length 820;
Best Local Similarity 100.0%; Pred. No. 4.6e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 60
Db 389 VHTKDIFNVKRCNGVVEEGEECDGPLKHCAKDPCCLSNCTLTGSGTCAFGLCCKDKCF 448

QY 61 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103
Db 449 LPSGKVCRCVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 5
US-09-792-200B-22
; Sequence 22, Application US/09792200B
; Patent No. US20020042368A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Fanslow, William C.
; APPLICANT: Poindexter, Kurt
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: INTEGRIN ANTAGONISTS
; FILE REFERENCE: 2958-A
; CURRENT APPLICATION NUMBER: US/09/792,200B
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/184,865
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-792-200B-22

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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:00:41 ; Search time 123 Seconds
(without alignments)
236.605 Million cell updates/sec

Title: US-10-664-456-12_COPY_389_491
Perfect score: 615
Sequence: 1 VHTKDIFNVKRCNGVVEEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	615	100.0	766	3	AAB07739	Aab07739 A snake v
2	615	100.0	787	3	AAB07740	Aab07740 A snake v
3	615	100.0	820	3	AAB07741	Aab07741 A snake v
4	557	90.6	528	4	AAE13061	Aae13061 ADAM-29di
5	446	72.5	726	2	AAY17413	Aay17413 Human SVP
6	446	72.5	726	2	AAY03223	Aay03223 Amino aci
7	446	72.5	726	7	ADC78877	Adc78877 Human PRO
8	446	72.5	776	6	ABR39425	AbR39425 Human GEN
9	443	72.0	542	2	AAY03224	Aay03224 Amino aci
10	443	72.0	722	2	AAY28655	Aay28655 Human SVP
11	443	72.0	722	6	ABG76200	Abg76200 Human sna
12	431	70.1	535	2	AAY17414	Aay17414 SVPH1-26
13	431	70.1	535	4	AAE13056	Aae13056 ADAM-20di
14	422	68.6	523	4	AAE13057	Aae13057 ADAM-21di
15	357	58.0	499	3	AAB07738	Aab07738 A snake v
16	357	58.0	781	3	AAB07743	Aab07743 A snake v
17	357	58.0	790	3	AAB07742	Aab07742 A snake v
18	357	58.0	790	3	AAB07705	Aab07705 Amino aci
19	357	58.0	790	4	AAU12273	Aau12273 Human PRO
20	357	58.0	790	6	ABO17717	AbO17717 Novel hum
21	357	58.0	790	6	ABU80971	Abu80971 Human PRO
22	357	58.0	790	6	ABU66671	Abu66671 Human PRO
23	357	58.0	790	6	ABU59752	Abu59752 Novel sec
24	357	58.0	790	6	ABO24942	AbO24942 Human sec
25	357	58.0	790	6	ABU66947	Abu66947 Human sec

26	357	58.0	790	6	ADA45723	Ada45723 Novel hum
27	357	58.0	790	6	ADA76154	Ada76154 Human PRO
28	357	58.0	790	6	ADA18804	Ada18804 Human PRO
29	357	58.0	790	6	ADA61427	Ada61427 Homo sapi
30	357	58.0	790	6	ADB19212	Adb19212 Novel hum
31	357	58.0	790	6	ADB27753	ADB27753 Human PRO
32	357	58.0	790	6	ADA86232	Ada86232 Novel hum
33	357	58.0	790	6	ADB15796	Adb15796 Human PRO
34	357	58.0	790	6	ADA47582	Ada47582 Human PRO
35	357	58.0	790	6	ADA67377	Ada67377 Human PRO
36	357	58.0	790	6	ADB30384	Adb30384 Human PRO
37	357	58.0	790	6	ADA85680	Ada85680 Novel hum
38	357	58.0	790	6	ADA96892	Ada96892 Human PRO
39	357	58.0	790	6	ADA79196	Ada79196 Human PRO
40	357	58.0	790	6	ADA87335	Ada87335 Novel hum
41	357	58.0	790	6	ADB16537	Adb16537 Human PRO
42	357	58.0	790	6	ADA91629	Ada91629 Novel hum
43	357	58.0	790	6	ADB14692	Adb14692 Human PRO
44	357	58.0	790	6	ADB18653	Adb18653 Novel hum
45	357	58.0	790	6	ADA93868	Ada93868 Human PRO

ALIGNMENTS

RESULT 1
AAB07739
ID AAB07739 standard; protein; 766 AA.
XX
AC AAB07739;
XX
DT 07-NOV-2000 (first entry)
XX
DE A snake venom protease (SVPH-1) polypeptide varaint SVPH-1a.
XX
KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;
KW chromosome 1; chromosome 4; immune system; splice variant.
XX
OS Homo sapiens.
XX
PN WO200043525-A2.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-US001338.
XX
PR 21-JAN-1999; 99US-0116670P.
PR 14-JUN-1999; 99US-0138682P.
PR 27-SEP-1999; 99US-0155798P.
(IMMV) IMMUNEX CORP.
PI Cerretti DP;
XX
DR WPI; 2000-482914/42.
DR N-PSDB; AAA59304.
XX
PT Snake venom protease (SVPH) nucleic acids, and polypeptides, used to
PT identify proteins having metalloproteinase-disintegrin activity, and
PT inhibitors of the proteins for use in therapeutics.
XX
PS Claim 13; Page 15; 105pp; English.
XX
CC The present sequence represnets an alternatively spliced snake venom
CC protease-1 (SVPH-1) polypeptide, designated SVPH-1a. The SVPH
CC polypeptides are metalloproteinase-disintegrin protein family members.
CC The SVPH polynucleotides can be used as probes to identify nucleic acids
CC encoding proteins having metalloproteinase-disintegrin activity, to
CC identify human chromosome 1 or 4, to map genes on those chromosomes, to
CC identify genes associated with diseases, syndromes and conditions
CC associated with the chromosomes, and to study proteinases and their
CC activities on cell/cell interactions and the immune system. Sense or
CC antisense oligonucleotides of SVPH can be used to inhibit gene expression

of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell and cell/matrix interactions involved in cellular processes and in the immune system. The polypeptides may also be used to screen for inhibitors of the polypeptide's activity, which are used in therapeutics. The antibodies can be used in assays to detect the presence of the polypeptides in vitro or in vivo, and to purify the polypeptides by affinity chromatography

SQ Sequence 766 AA;
Query Match 100.0%; Score 615; DB 3; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.9e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 2
AAB07740
ID AAB07740 standard; protein: 787 AA.

AC AAB07740;

DT 07-NOV-2000 (first entry)

DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1b.

Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin; KW
chromosome 1; chromosome 4; immune system; splice variant. KW

OS Homo sapiens.

PN WO200043525-A2.

PD 27-JUL-2000.

PF 21-JAN-2000; 2000WO-US001338.

PR 21-JAN-1999; 99US-0116670P.

PR 27-SEP-1999; 99US-0155798P.

PA (IMMV) IMMUNEX CORP.

PI Cerretti DP;

DR WPI; 2000-48

XX

PT identify proteins

xx
ps Claim 13; Page 15-16; 105pp; English.

CC The present sequence represents an al

polypeptides are metalloproteinase-disintegrin protein family members. The SVPH polynucleotides can be used as probes to identify nucleic acids encoding proteins having metalloproteinase-disintegrin activity, to identify human chromosome 1 or 4, to map genes on those chromosomes, to identify genes associated with diseases, syndromes and conditions associated with the chromosomes, and to study proteinases and their activities on cell/cell interactions and the immune system. Sense or antisense oligonucleotides of SVPH can be used to inhibit gene expression of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell and cell/matrix interactions involved in cellular processes and in the

immune system. The polypeptides may also be used to screen for inhibitors of the polypeptide's activity, which are used in therapeutics. The antibodies can be used in assays to detect the presence of the polypeptides in vitro or in vivo, and to purify the polypeptides by affinity chromatography

Query Match	100.0%;	Score 615;	DB 3;	Length 787;
Best Local Similarity	100.0%;	Pred. No. 7.1e-43;		
Matches 103; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

1	VHTKDIFNVKRCGNGVVEEGEECD	CGPLKHCAKDPCLSLNCTLT	DGSTCAFGLCCKDKCF	60
389	VHTKDIFNVKRCGNGVVEEGEECD	CGPLKHCAKDPCLSLNCTLT	DGSTCAFGLCCKDKCF	448
61	LPSGKVCRKVEKNECDLPWCNGT	SHKCPDDFYVEDGIPCKERG	103	
449	LPSGKVCRKVEKNECDLPWCNGT	SHKCPDDFYVEDGIPCKERG	491	

RESULT 3
AAB07741
ID AAB07741 standard; protein; 820 AA.

AC AAB07741;

DT 07-NOV-2000 (first entry)

DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1c.

KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;
KW chromosome 1; chromosome 4; immune system; splice variant.

OS Homo sapiens.

PN WO200043525-A2.

PD 27-JUL-2000.

21-JAN-2000; 2000WO-US001338.

PR 21-JAN-1999; 99US-0116670P.

PR 27-SEP-1999; 99US-0155798P.

PA (IMMV) IMMUNEX CORP.

PI Cerretti DP;

DR WPI; 2000-48

PT identify proteins

PS Claim 13; Page 16; 105pp; English.

CC The present sequence represents an

polypeptides are metalloproteinase-disintegrin protein family members. The SVPH polynucleotides can be used as probes to identify nucleic acids encoding proteins having metalloproteinase-disintegrin activity, to identify human chromosome 1 or 4, to map genes on those chromosomes, to identify genes associated with diseases, syndromes and conditions associated with the chromosomes, and to study proteinases and their activities on cell/cell interactions and the immune system. Sense or antisense oligonucleotides of SVPH can be used to inhibit gene expression of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell and cell/matrix interactions involved in cellular processes and in the immune system. The polypeptides may also be used to screen for inhibitors of the polypeptide's activity, which are used in therapeutics. The

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:08:28 ; Search time 23 Seconds
(without alignments)
233.184 Million cell updates/sec

Title: US-10-664-456-12_COPY_389_491
Perfect score: 615
Sequence: 1 VHTKDIENVKRCNGWVEEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615	100.0	820	1 AD29_HUMAN	Q9ukf5 homo sapien
2	446	72.5	726	1 AD20_HUMAN	O43506 homo sapien
3	443	72.0	722	1 AD21_HUMAN	Q9ukj8 homo sapien
4	408	66.3	729	1 AD21_MOUSE	Q9ji76 mus musculu
5	404	65.7	760	1 AD25_MOUSE	Q9r159 mus musculu
6	382	62.1	697	1 AD26_MOUSE	Q9r158 mus musculu
7	357	58.0	790	1 AD30_HUMAN	Q9ukf2 homo sapien
8	351.5	57.2	761	1 AD24_MOUSE	Q9r160 mus musculu
9	314	51.1	920	1 AD19_MOUSE	O35674 mus musculu
10	309	50.2	956	1 AD19_HUMAN	Q9h013 homo sapien
11	306.5	49.8	819	1 AD09_HUMAN	Q13443 homo sapien
12	294	47.8	903	1 AD12_MOUSE	Q61824 mus musculu
13	291.5	47.4	745	1 AD02_BOVIN	O77780 bos taurus
14	289	47.0	813	1 AD33_HUMAN	Q9b211 homo sapien
15	283	46.0	909	1 AD12_HUMAN	O43184 homo sapien
16	276.5	45.0	797	1 AD33_MOUSE	Q923w9 mus musculu
17	274	44.6	791	1 AD1A_MOUSE	Q60813 mus musculu
18	273.5	44.5	935	1 AD22_XENLA	O42596 xenopus lae
19	272	44.2	789	1 AD01_RAT	P70505 rattus norv
20	268.5	43.7	735	1 AD02_MOUSE	Q60718 mus musculu
21	265.5	43.2	857	1 AD22_MOUSE	Q9r1v6 mus musculu
22	264.5	43.0	906	1 AD22_HUMAN	Q9p0k1 homo sapien
23	263.5	42.8	735	1 AD02_HUMAN	Q99965 homo sapien
24	263.5	42.8	751	1 AD02_RABIT	Q28660 oryctolagus
25	263	42.8	824	1 AD08_HUMAN	P78325 homo sapien
26	262.5	42.7	737	1 AD02_RAT	Q63202 rattus norv
27	261.5	42.5	452	1 AD11_XENLA	Q9psz3 xenopus lae
28	261	42.4	735	1 AD02_CAVPO	Q60411 cavia porce
29	261	42.4	769	1 AD11_HUMAN	O75078 homo sapien
30	261	42.4	773	1 AD11_MOUSE	Q9r1v4 mus musculu
31	260.5	42.4	735	1 AD02_MACFA	Q28478 macaca fasc
32	259	42.1	754	1 AD07_HUMAN	Q9h2u9 homo sapien
33	257	41.8	775	1 AD28_HUMAN	Q9ukq2 homo sapien

RESULT 1									
AD29_HUMAN									
ID	AD29_HUMAN	STANDARD;	PRT;	820	AA.				
AC	Q9UKF5; Q9UHP1; Q9UKF3; Q9UKF4;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	15-MAR-2004 (Rel. 43, Last annotation update)								
DE	ADAM 29 precursor (A disintegrin and metalloproteinase domain 29).								
GN	ADAM29.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).								
RC	TISSUE=Testis;								
RX	MEDLINE=99443746; PubMed=10512762;								
RA	Cerretti D.P., DuBose R.F., Black R.A., Nelson N.;								
RT	"Isolation of two novel metalloproteinase-disintegrin (ADAM) cDNAs that show testis-specific gene expression.";								
RL	Biochem. Biophys. Res. Commun. 263:810-815(1999).								
RN	[2]								
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).								
RC	TISSUE=Testis;								
RX	MEDLINE=20112771; PubMed=10644455;								
RA	Xu R., Cai J., Xu T., Zhou W., Ying B., Deng K., Zhao S., Li C.;								
RT	"Molecular cloning and mapping of a novel ADAM gene (ADAM29) to human chromosome 4.";								
RL	Genomics 62:537-539(1999).								
CC	-!- FUNCTION: May be involved in spermatogenesis and fertilization.								
CC	Seems to be a non catalytic metalloprotease-like protein.								
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.								
CC	-!- ALTERNATIVE PRODUCTS:								
CC	Event=Alternative splicing; Named isoforms=3;								
CC	Name=Alpha;								
CC	ISoId=Q9UKF5-1; Sequence=Displayed;								
CC	Name=Beta;								
CC	ISoId=Q9UKF5-2; Sequence=VSP_005491;								
CC	Name=Gamma;								
CC	ISoId=Q9UKF5-3; Sequence=VSP_005492, VSP_005493;								
CC	TISSUE SPECIFICITY: Expressed specifically in testes.								
CC	-!- SIMILARITY: Contains 1 EGF-like domain.								
CC	-!- SIMILARITY: Contains 1 disintegrin domain.								
CC	-!- SIMILARITY: Belongs to peptidase family M12B.								
CC	-----								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; AF171929; AAF03777.1; --								
DR	EMBL; AF171930; AAF03778.1; --								
DR	EMBL; AF171931; AAF03779.1; --								

34	257	41.8	776	1	AD07_MACFA	Q28475 macaca fasc
35	256	41.6	826	1	AD08_MOUSE	Q05910 mus musculu
36	254	41.3	776	1	AD28_MACFA	Q9xsl6 macaca fasc
37	254	41.3	806	1	AD1B_MOUSE	Q8r534 mus musculu
38	253	41.1	789	1	AD07_RAT	Q63180 rattus norv
39	252	41.0	788	1	AD07_MOUSE	O35227 mus musculu
40	251	40.8	571	1	DISJ_BOTJA	P30431 bothrops ja
41	250.5	40.7	512	1	YE94_SCHPO	O13766 schizosacch
42	245.5	39.9	814	1	AD15_HUMAN	Q13444 homo sapien
43	240.5	39.1	864	1	AD15_MOUSE	O88839 mus musculu
44	237.5	38.6	816	1	AD15_RAT	Q9gyv0 r adam 15 p
45	235	38.2	793	1	AD28_MOUSE	Q9jln6 mus musculu

ALIGNMENTS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:11:58 ; Search time 33 Seconds
(without alignments)
161.136 Million cell updates/sec

Title: US-10-664-456-12_COPY_389_491
Perfect score: 615
Sequence: 1 VHTKIDFNVKRCNGVVEEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	443	72.0	722	4	US-09-617-145-2 Sequence 2, Appli
2	309	50.2	751	2	US-08-836-443-3 Sequence 3, Appli
3	289	47.0	746	4	US-09-548-797B-4 Sequence 4, Appli
4	289	47.0	787	4	US-09-548-797B-5 Sequence 5, Appli
5	289	47.0	802	4	US-09-632-098-2 Sequence 2, Appli
6	289	47.0	812	4	US-09-632-098-4 Sequence 4, Appli
7	289	47.0	849	4	US-09-548-797B-6 Sequence 6, Appli
8	268.5	43.7	457	1	US-08-264-101-4 Sequence 4, Appli
9	268.5	43.7	457	2	US-08-765-243-4 Sequence 4, Appli
10	268.5	43.7	457	5	PCT-US95-07295-4 Sequence 4, Appli
11	268.5	43.7	735	2	US-08-765-243-6 Sequence 6, Appli
12	268.5	43.7	735	5	PCT-US95-07295-6 Sequence 6, Appli
13	263.5	42.8	651	1	US-08-264-101-2 Sequence 2, Appli
14	263.5	42.8	651	2	US-08-765-243-2 Sequence 2, Appli
15	263.5	42.8	651	5	PCT-US95-07295-2 Sequence 2, Appli
16	263.5	42.8	734	2	US-08-765-243-8 Sequence 8, Appli
17	263.5	42.8	734	5	PCT-US95-07295-8 Sequence 8, Appli
18	261	42.4	488	1	US-08-243-542-1 Sequence 1, Appli
19	261	42.4	488	1	US-08-477-407-1 Sequence 1, Appli
20	261	42.4	488	1	US-08-484-355-1 Sequence 1, Appli
21	261	42.4	524	1	US-08-243-542-2 Sequence 2, Appli
22	261	42.4	524	1	US-08-477-407-2 Sequence 2, Appli
23	261	42.4	524	1	US-08-484-355-2 Sequence 2, Appli
24	261	42.4	670	1	US-08-243-542-3 Sequence 3, Appli
25	261	42.4	670	1	US-08-477-407-3 Sequence 3, Appli
26	261	42.4	670	1	US-08-484-355-3 Sequence 3, Appli
27	261	42.4	769	1	US-08-243-542-4 Sequence 4, Appli

28	261	42.4	769	1	US-08-477-407-4 Sequence 4, Appli
29	261	42.4	769	1	US-08-484-355-4 Sequence 4, Appli
30	257	41.8	540	4	US-09-786-256C-1 Sequence 1, Appli
31	257	41.8	540	4	US-09-786-256C-30 Sequence 30, Appli
32	257	41.8	775	4	US-09-786-256C-15 Sequence 15, Appli
33	257	41.8	775	4	US-09-786-256C-32 Sequence 32, Appli
34	245.5	39.9	814	3	US-09-813-819-4 Sequence 4, Appli
35	245.5	39.9	814	4	US-09-920-048-4 Sequence 4, Appli
36	245.5	39.9	855	3	US-09-813-819-2 Sequence 2, Appli
37	245.5	39.9	855	4	US-09-920-048-2 Sequence 2, Appli
38	241	39.2	96	4	US-09-786-256C-2 Sequence 2, Appli
39	241	39.2	696	3	US-09-351-414-2 Sequence 2, Appli
40	239	38.9	529	2	US-08-836-442-3 Sequence 3, Appli
41	237	38.5	621	4	US-09-026-001A-6 Sequence 6, Appli
42	235.5	38.3	781	4	US-09-738-946-8 Sequence 8, Appli
43	232	37.7	613	4	US-09-026-001A-10 Sequence 10, Appli
44	232	37.7	621	4	US-09-026-001A-18 Sequence 18, Appli
45	229	37.2	616	4	US-09-608-790-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-617-145-2
; Sequence 2, Application US/09617145
; Patent No. 6485956
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVPH1-8 DNA and Polypeptides
; FILE REFERENCE: 03260.0050-00304
; CURRENT APPLICATION NUMBER: US/09/617,145
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/071,505
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-145-2

Query Match	72.0%;	Score 443;	DB 4;	Length 722;
Best Local Similarity	71.1%;	Pred. No. 4.1e-32;		
Matches	69;	Conservative	15;	Mismatches 13; Indels 0; Gaps 0;
QY	5	DIFNVKRCNGVVEEGEECDGGLKHKCAKDPCCLSNCTLTGSTCAFGLCKCKDCKFLPSG	64	
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Db	402	EIFMLKRCNGVVEEREEQCDCGVSQQCEQDACLLNCTLRPGAACAFGLCKCKCKFMPFSG	461	
QY	65	KVCRKEVNECDLPEWNCNGTSHKCPDDFYVEDGIPCKE	101	
		: :	: :	: :
Db	462	ELCRQEVNECDLPEWNCNGTSHQCPEDRYVQDGIPCS	498	
RESULT 2				
US-08-836-443-3				
; Sequence 3, Application US/08836443				
; Patent No. 5883241				
; GENERAL INFORMATION:				
; APPLICANT: DOCHERTY, Andrew, J.P				
; APPLICANT: SLOCOMBE, Patrick, M.				
; TITLE OF INVENTION: DNA SEQUENCES CODING FOR A				
; TITLE OF INVENTION: HUMAN METALLOPROTEINASE AND VARIANTS THEREOF				
; NUMBER OF SEQUENCES: 4				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP.				
; STREET: 130 Water Street				
; CITY: Boston				
; STATE: MA				
; COUNTRY: USA				
; ZIP: 02109				

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OM protein - protein search, using sw model

Run on: August 27, 2004, 22:01:22 ; Search time 116 Seconds
(without alignments)
280.158 Million cell updates/sec

Title: US-10-664-456-12_COPY_389_491
Perfect score: 615
Sequence: 1 VHTKDI FNVKRCGNGVVEG.....SHKCPDDFYVEDGIPCKERG 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	73.0	763	11 Q811Q4	Q811Q4 mus musculus
2	386	62.8	697	11 Q8BMR4	Q8bmr4 mus musculus
3	382	62.1	702	11 Q8BMR5	Q8bmr5 mus musculus
4	382	62.1	714	11 Q8K4K0	Q8k4k0 mus musculus
5	357	58.0	790	4 Q8TBZ7	Q8tbz7 homo sapien
6	353.5	57.5	761	11 Q8CDV3	Q8cdv3 mus musculus
7	340	55.3	732	11 Q811Q3	Q811q3 mus musculus
8	325	52.8	203	11 P97777	P97777 rattus norv
9	316.5	51.5	845	11 Q61072	Q61072 mus musculus
10	316.5	51.5	853	11 Q80U94	Q8ou94 mus musculus
11	314	51.1	473	11 Q60815	Q60815 mus musculus
12	314	51.1	763	11 Q8CGQ2	Q8cgq2 mus musculus
13	312	50.7	703	11 Q8C0V3	Q8c0v3 mus musculus
14	311	50.6	730	6 O19051	O19051 oryctolagus
15	307.5	50.0	873	13 O42595	O42595 xenopus lae
16	306.5	49.8	655	4 Q8NFM6	Q8nfm6 homo sapien

17	305.5	49.7	732	6 Q28484	Q28484 macaca fasc
18	304	49.4	731	6 O19050	O19050 oryctolagus
19	303	49.3	754	11 Q8CGQ1	Q8cgq1 mus musculu
20	298.5	48.5	735	6 Q866A8	Q866a8 sus scrofa
21	298	48.5	751	11 P70535	P70535 rattus norv
22	293	47.6	713	6 Q28485	Q28485 macaca fasc
23	289	47.0	474	6 Q95LW7	Q95lw7 macaca fasc
24	289	47.0	735	11 Q60473	Q60473 cavia porce
25	289	47.0	812	4 Q8NOW6	Q8now6 homo sapien
26	289	47.0	919	6 Q28659	Q28659 oryctolagus
27	284	46.2	914	13 O12960	O12960 xenopus lae
28	282	45.9	825	6 Q28477	Q28477 macaca fasc
29	282	45.9	838	6 O19056	O19056 papio anubi
30	282	45.9	899	13 Q8UVF1	Q8uvf1 coturnix co
31	282	45.9	905	6 Q28476	Q28476 macaca fasc
32	281	45.7	825	6 O46652	O46652 papio anubi
33	280	45.5	792	6 O19061	O19061 saguinus oe
34	280	45.5	804	11 Q60410	Q60410 cavia porce
35	276.5	45.0	797	11 Q8R465	Q8r465 mus musculu
36	276.5	45.0	797	11 Q8R5G5	Q8r5g5 mus musculu
37	273.5	44.5	706	13 O42593	O42593 xenopus lae
38	273	44.4	612	13 Q7T046	Q7t046 vipera lebe
39	272	44.2	697	13 Q7ZY29	Q7zy29 brachydanio
40	271	44.1	1023	5 Q967H9	Q967h9 strongyloce
41	265.5	43.2	694	5 Q9GZ15	Q9gz15 drosophila
42	265.5	43.2	1182	5 Q9VXL1	Q9vxl1 drosophila
43	265	43.1	821	6 O19060	O19060 saguinus oe
44	265	43.1	836	6 O19057	O19057 pongo pygma
45	264	42.9	612	13 Q8UVG0	Q8uvg0 bothrops er

ALIGNMENTS

RESULT 1
Q811Q4 PRELIMINARY; PRT; 763 AA.
ID Q811Q4
AC Q811Q4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ADAM29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Testis;
RA Choi I., Cho C.;
RT "Cloning and characterization of ADAM29.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY190759; AA038663.1; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000564; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
SQ SEQUENCE 763 AA; 86444 MW; F9EF082C3BFBA80 CRC64;

Query Match 73.0%; Score 449; DB 11; Length 763;
Best Local Similarity 72.7%; Pred. No. 2.5e-45;

